(19) Europäisches Patentamt
European Patent Office
Office européen des brevets

(11) Publication number: **0 399 666**
A1

(12) **EUROPEAN PATENT APPLICATION**

(21) Application number: **90304575.5**

(51) Int. Cl.5: **C12N 15/62, C07K 13/00, C12P 21/02**

(22) Date of filing: **26.04.90**

The title of the invention has been amended (Guidelines for Examination in the EPO, A-III, 7.3).

(30) Priority: **29.04.89 GB 8909919**

(43) Date of publication of application: **28.11.90 Bulletin 90/48**

(84) Designated Contracting States: **ES GR**

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(54) **Fusion proteins containing N-terminal fragments of human serum albumin.**

(57) A fusion polypeptide comprising, as at least part of the N-terminal portion thereof, an N-terminal portion of HSA or a variant thereof and, as at least part of the C-terminal portion thereof, another polypeptide except that, when the said N-terminal portion of HSA is the 1-n portion where n is 369 to 419 or a variant thereof then the said polypeptide is one of various specified entities, including the 585 to 1578 portion of human fibronectin or a variant thereof.

The HSA-like portion may have additional N-terminal residues, such as secretion leader sequences (signal sequences). The C-terminal portion is preferably the 585-1578 portion of human plasma fibronectin. The N-terminal and C-terminal portions may be cleavable to yield the isolated C-terminal portion, with the N-terminal portion having served to facilitate secretion from the host.

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POLYPEPTIDES

The present invention relates to fusion polypeptides where two individual polypeptides or parts thereof are fused to form a single amino acid chain. Such fusion may arise from the expression of a single continuous coding sequence formed by recombinant DNA techniques.

Fusion polypeptides are known, for example those where a polypeptide which is the ultimately desired product of the process is expressed with an N-terminal "leader sequence" which encourages or allows secretion of the polypeptide from the cell. An example is disclosed in EP-A-116 201 (Chiron).

Human serum albumin (HSA) is a known protein found in the blood. EP-A-147 198 (Delta Biotechnology) discloses its expression in a transformed host, in this case yeast. Our earlier application EP-A-322 094 discloses N-terminal fragments of HSA, namely those consisting of residues 1-n where n is 369 to 419, which have therapeutic utility. The application also mentions the possibility of fusing the C-terminal residue of such molecules to other, unnamed, polypeptides.

One aspect of the present invention provides a fusion polypeptide comprising, as at least part of the N-terminal portion thereof, an N-terminal portion of HSA or a variant thereof and, as at least part of the C-terminal portion thereof, another polypeptide except that, when the said N-terminal portion of HSA is the 1-n portion where n is 369 to 419 or a variant thereof then the said polypeptide is (a) the 585 to 1578 portion of human fibronectin or a variant thereof, (b) the 1 to 368 portion of CD4 or a variant thereof, (c) platelet derived growth factor, or a variant thereof, (d) transforming growth factor, or a variant thereof, (e) the 1-261 portion of mature human plasma fibronectin or a variant thereof, (f) the 278-578 portion of mature human plasma fibronectin or a variant thereof, (g) the 1-272 portion of mature human von Willebrand's Factor or a variant thereof, or (h) alpha-1-antitrypsin or a variant thereof.

The N-terminal portion of HSA is preferably the said 1-n portion, the 1-177 portion (up to and including the cysteine), the 1-200 portion (up to but excluding the cysteine) or a portion intermediate 1-177 and 1-200.

The term "human serum albumin" (HSA) is intended to include (but not necessarily to be restricted to) known or yet-to-be-discovered polymorphic forms of HSA. For example, albumin Naskapi has Lys-372 in place of Glu-372 and pro-albumin Christchurch has an altered pro-sequence. The term "variants" is intended to include (but not necessarily to be restricted to) minor artificial variations in sequence (such as molecules lacking one or a few residues, having conservative substitutions or minor insertions of residues, or having minor variations of amino acid structure). Thus polypeptides which have 80%, preferably 85%, 90%, 95% or 99%, homology with HSA are deemed to be "variants". It is also preferred for such variants to be physiologically equivalent to HSA; that is to say, variants preferably share at least one pharmacological utility with HSA. Furthermore, any putative variant which is to be used pharmacologically should be non-immunogenic in the animal (especially human) being treated.

Conservative substitutions are those where one or more amino acids are substituted for others having similar properties such that one skilled in the art of polypeptide chemistry would expect at least the secondary structure, and preferably the tertiary structure, of the polypeptide to be substantially unchanged. For example, typical such substitutions include asparagine for glutamine, serine for asparagine and arginine for lysine. Variants may alternatively, or as well, lack up to ten (preferably only one or two) intermediate amino acid residues (ie not at the termini of the said N-terminal portion of HSA) in comparison with the corresponding portion of natural HSA; preferably any such omissions occur in the 100 to 369 portion of the molecule (relative to mature HSA itself) (if present). Similarly, up to ten, but preferably only one or two, amino acids may be added, again in the 100 to 369 portion for preference (if present). The term "physiologically functional equivalents" also encompasses larger molecules comprising the said sequence plus a further sequence at the N-terminal (for example, pro-HSA, pre-pro-HSA and met-HSA).

Clearly, the said "another polypeptide" in the fusion compounds of the invention cannot be the remaining portion of HSA, since otherwise the whole polypeptide would be HSA, which would not then be a "fusion polypeptide".

Even when the HSA-like portion is not the said 1-n portion of HSA, it is preferred for the non-HSA portion to be one of the said (a) to (h) entities.

The 1 to 368 portion of CD4 represents the first four disulphide-linked immunoglobulin-like domains of the human T lymphocyte CD4 protein, the gene for and amino acid sequence of which are disclosed in D. Smith et al (1987) Science 328, 1704-1707. It is used to combat HIV infections.

The sequence of human platelet-derived growth factor (PDGF) is described in Collins et al (1985) Nature 316, 748-750. Similarly, the sequence of transforming growth factors β (TGF-β) is described in Derynck et al (1985) Nature 316, 701-705. These growth factors are useful for wound-healing.

A cDNA sequence for the 1-261 portion of Fn was disclosed in EP-A-207 751 (obtained from plasmid pFH6 with endonuclease PvuII). This portion binds fibrin and can be used to direct fused compounds to blood clots.

A cDNA sequence for the 278-578 portion of Fn, which contains a collagen-binding domain, was disclosed by R.J. Owens and F.E. Baralle in 1986 E.M.B.O.J. 5, 2825-2830. This portion will bind to platelets.

The 1-272 portion of von Willebrand's Factor binds and stabilises factor VIII. The sequence is given in Bontham et al, Nucl. Acids Res. 14, 7125-7127.

Variants of alpha-1-antitrypsin include those disclosed by Rosenburg et al (1984) Nature 312, 77-80. In particular, the present invention includes the Pittsburgh variant (Met^{358} is mutated to Arg) and the variant where Pro^{357} and Met^{358} are mutated to alanine and arginine respectively. These compounds are useful in the treatment of septic shock and lung disorders.

Variants of the non-HSA portion of the polypeptides of the invention include variations as discussed above in relation to the HSA portion, including those with conservative amino acid substitutions, and also homologues from other species.

The fusion polypeptides of the invention may have N-terminal amino acids which extend beyond the portion corresponding to the N-terminal portion of HSA. For example, if the HSA-like portion corresponds to an N-terminal portion of mature HSA, then pre-, pro-, or pre-pro sequences may be added thereto, for example the yeast alpha-factor leader sequence. The fused leader portions of WO 90/01063 may be used. The polypeptide which is fused to the HSA portion may be a naturally-occurring polypeptide, a fragment thereof or a novel polypeptide, including a fusion polypeptide. For example, in Example 3 below, a fragment of fibronectin is fused to the HSA portion via a 4 amino acid linker.

It has been found that the amino terminal portion of the HSA molecule is so structured as to favour particularly efficient translocation and export of the fusion compounds of the invention in eukaryotic cells.

A second aspect of the invention provides a transformed host having a nucleotide sequence so arranged as to express a fusion polypeptide as described above. By "so arranged", we mean, for example, that the nucleotide sequence is in correct reading frame with an appropriate RNA polymerase binding site and translation start sequence and is under the control of a suitable promoter. The promoter may be homologous with or heterologous to the host. Downstream (3′) regulatory sequences may be included if desired, as is known. The host is preferably yeast (for example Saccharomyces spp., e.g. S. cerevisiae; Kluyveromyces spp., e.g. K. lactis; Pichia spp.; or Schizosaccharomyces spp., e.g. S. pombe) but may be any other suitable host such as E. coli, B. subtilis, Aspergillus spp., mammalian cells, plant cells or insect cells.

A third aspect of the invention provides a process for preparing a fusion polypeptide according to the first aspect of the invention by cultivation of a transformed host according to the second aspect of the invention, followed by separation of the fusion polypeptide in a useful form.

A fourth aspect of the invention provides therapeutic methods of treatment of the human or other animal body comprising administration of such a fusion polypeptide.

In the methods of the invention we are particularly concerned to improve the efficiency of secretion of useful therapeutic human proteins from yeast and have conceived the idea of fusing to amino-terminal portions of HSA those proteins which may ordinarily be only inefficiently secreted. One such protein is a potentially valuable wound-healing polypeptide representing amino acids 585 to 1578 of human fibronectin (referred to herein as Fn 585-1578). As we have described in a separate application (filed simultaneously herewith) this molecule contains cell spreading, chemotactic and chemokinetic activities useful in healing wounds. The fusion polypeptides of the present invention wherein the C-terminal portion is Fn 585-1578 can be used for wound healing applications as biosynthesised, especially where the hybrid human protein will be topically applied. However, the portion representing amino acids 585 to 1578 of human fibronectin can if desired be recovered from the fusion protein by preceding the first amino acid of the fibronectin portion by amino acids comprising a factor X cleavage site. After isolation of the fusion protein from culture supernatant, the desired molecule is released by factor X cleavage and purified by suitable chromatography (e.g. ion-exchange chromatography). Other sites providing for enzymatic or chemical cleavage can be provided, either by appropriate juxtaposition of the N-terminal and C-terminal portions or by the insertion therebetween of an appropriate linker.

At least some of the fusion polypeptides of the invention, especially those including the said CD4 and vWF fragments, PDGF and α_1AT, also have an increased half-life in the blood and therefore have advantages and therapeutic utilities themselves, namely the therapeutic utility of the non-HSA portion of the molecule. In the case of α_1AT and others, the compound will normally be administered as a one-off dose or only a few doses over a short period, rather than over a long period, and therefore the compounds are less

likely to cause an immune response.

EXAMPLES : SUMMARY

Standard recombinant DNA procedures were as described by Maniatis et al (1982 and recent 2nd edition) unless otherwise stated. Construction and analysis of phage M13 recombinant clones was as described by Messing (1983) and Sanger et al (1977).

DNA sequences encoding portions of human serum albumin used in the construction of the following molecules are derived from the plasmids mHOB12 and pDBD2 (EP-A-322 094, Delta Biotechnology Ltd, relevant portions of which are reproduced below) or by synthesis of oligonucleotides equivalent to parts of this sequence. DNA sequences encoding portions of human fibronectin are derived from the plasmid pFHDEL1, or by synthesis of oligonucleotides equivalent to parts of this sequence. Plasmid pFHDEL1, which contains the complete human cDNA encoding plasma fibronectin, was obtained by ligation of DNA derived from plasmids pFH6, 16, 54, 154 and 1 (EP-A-207 751; Delta Biotechnology Ltd).

This DNA represents an mRNA variant which does not contain the 'ED' sequence and had an 89-amino acid variant of the III-CS region (R.J. Owens, A.R. Kornblihtt and F.E. Baralle (1986) Oxford Surveys on Eukaryotic Genes 3 141-160). The map of this vector is disclosed in Fig. 11 and the protein sequence of the mature polypeptide produced by expression of this cDNA is shown in Fig. 5.

Oligonucleotides were synthesised on an Applied Biosystems 380B oligonucleotide synthesiser according to the manufacturer's recommendations (Applied Biosystems, Warrington, Cheshire, UK).

An expression vector was constructed in which DNA encoding the HSA secretion signal and mature HSA up to and including the 387th amino acid, leucine, fused in frame to DNA encoding a segment of human fibronectin representing amino acids 585 to 1578 inclusive, was placed downstream of the hybrid promoter of EP-A-258 067 (Delta Biotechnology), which is a highly efficient galactose-inducible promoter functional in Saccharomyces cerevisiae. The codon for the 1578th amino acid of human fibronectin was directly followed by a stop codon (TAA) and then the S. cerevisiae phosphoglycerate kinase (PGK) gene transcription terminator. This vector was then introduced into S. cerevisiae by transformation, wherein it directed the expression and secretion from the cells of a hybrid molecule representing the N-terminal 387 amino acids of HSA C-terminally fused to amino acids 585 to 1578 of human fibronectin.

In a second example a similar vector is constructed so as to enable secretion by S. cerevisiae of a hybrid molecule representing the N-terminal 195 amino acids of HSA C-terminally fused to amino acids 585 to 1578 of human fibronectin.

Aspects of the present invention will now be described by way of example and with reference to the accompanying drawings, in which:

Figure 1 (on two sheets) depicts the amino acid sequence currently thought to be the most representative of natural HSA, with (boxed) the alternative C-termini of HSA(1-n);

Figure 2 (on two sheets) depicts the DNA sequence coding for mature HSA, wherein the sequence included in Linker 3 is underlined;

Figure 3 illustrates, diagrammatically, the construction of mHOB16;

Figure 4 illustrates, diagrammatically, the construction of pHOB31;

Figure 5 (on 6 sheets) illustrates the mature protein sequence encoded by the Fn plasmid pFHDEL1;

Figure 6 illustrates Linker 5, showing the eight constituent oligonucleotides;

Figure 7 shows schematically the construction of plasmid pDBDF2;

Figure 8 shows schematically the construction of plasmid pDBDF5;

Figure 9 shows schematically the construction of plasmid pDBDF9;

Figure 10 shows schematically the construction of plasmid DBDF12, using plasmid pFHDEL1; and

Figure 11 shows a map of plasmid pFHDEL1.

EXAMPLE 1 : HSA 1-387 FUSED TO Fn 585-1578

The following is an account of a preparation of plasmids comprising sequences encoding a portion of HSA, as is disclosed in EP-A-322 094.

The human serum albumin coding sequence used in the construction of the following molecules is derived from the plasmid M13mp19.7 (EP-A-201 239, Delta Biotech- nology Ltd.) or by synthesis of oligonucleotides equivalent to parts of this sequence. Oligonucleotides were synthesised using phosphoramidite chemistry on an Applied Biosystems 380B oligonucleotide synthesizer according to the

manufacturer's recommendations (AB Inc., Warrington, Cheshire, England).

An oligonucleotide was synthesised (Linker A) which represented a part of the known HSA coding sequence (Figure 2) from the PstI site (1235-1240, Figure 2) to the codon for valine 381 wherein that codon was changed from GTG to GTC:

Linker 1

```
                  D     P     H     E     C     Y
5'               GAT   CCT   CAT   GAA   TGC   TAT
3'  ACGT         CTA   GGA   GTA   CTT   ACG   ATA
                             1247

A     K     V     F     D     E     F     K
GCC   AAA   GTG   TTC   GAT   GAA   TTT   AAA
CGG   TTT   CAC   AAG   CTA   CTT   AAA   TTT
            1267
P     L     V'
CTT   GTC    3'
GGA   CAG    5'
```

Linker 1 was ligated into the vector M13mp19 (Norrander et al, 1983) which had been digested with PstI and HincII and the ligation mixture was used to transfect E.coli strain XL1-Blue (Stratagene Cloning Systems, San Diego, CA). Recombinant clones were identified by their failure to evolve a blue colour on medium containing the chromogenic indicator X-gal (5-bromo-4-chloro-3-indolyl-β-D-galactoside) in the present of IPTG (isopropylthio-β-galactoside). DNA sequence analysis of template DNA prepared from bacteriophage particles of recombinant clones identified a molecule with the required DNA sequence, designated mHOB12 (Figure 3). M13mp19.7 consists of the coding region of mature HSA in M13mp19 (Norrander et al, 1983) such that the codon for the first amino acid of HSA, GAT, overlaps a unique XhoI site thus:

```
                    Asp   Ala
5'    C T C G A G A T G C A     3'
3'    G A G C T C T A C G T     5'
        XhoI
```

(EP-A-210 239). M13mp19.7 was digested with XhoI and made flush-ended by S1-nuclease treatment and was then ligated with the following oligonucleotide (Linker 2):

Linker 2

```
5' T C T T T T A T C C A A G C T T G G A T A A A A G A  3'
3' A G A A A A T A G G T T C G A A C C T A T T T T C T  5'
                        HindIII
```

The ligation mix was then used to transfect E.coli XL1-Blue and template DNA was prepared from several plaques and then analysed by DNA sequencing to identify a clone, pDBD1 (Figure 4), with the correct sequence.

A 1.1 kb HindIII to PstI fragment representing the 5′ end of the HSA coding region and one half of the inserted oligonucleotide linker was isolated from pDBD1 by agarose gel electrophoresis. This fragment was then ligated with double stranded mHOB12 previously digested with HindIII and PstI and the ligation mix was then used to transfect E.coli XL1-Blue. Single stranded template DNA was prepared from mature bacteriophage particles of several plaques. The DNA was made double stranded in vitro by extension from annealed sequencing primer with the Klenow fragment of DNA polymerase I in the presence of deoxynucleoside triphosphates. Restriction enzyme analysis of this DNA permitted the identification of a clone with the correct configuration, mHOB15 (Figure 4).

The following oligonucleotide (Linker 3) represents from the codon for the 382nd amino acid of mature HSA (glutamate, GAA) to the codon for lysine 389 which is followed by a stop codon (TAA) and a HindIII site and then a BamHI cohesive end:

Linker 3

```
    E   E   P   Q   N   L   I   K   J
5' GAA GAG CCT CAG AAT TTA ATC AAA TAA GCTTG      3'
3' CTT CTC GGA GTC TTA AAT TAG TTT ATT CGAACCTAG  5'
```

This was ligated into double stranded mHOB15, previously digested with HincII and BamHI. After ligation, the DNA was digested with HincII to destroy all non-recombinant molecules and then used to transfect E.coli XL1-Blue. Single stranded DNA was prepared from bacteriophage particles of a number of clones and subjected to DNA sequence analysis. One clone having the correct DNA sequence was designated mHOB16 (Figure 4).

A molecule in which the mature HSA coding region was fused to the HSA secretion signal was created by insertion of Linker 4 into BamHI and XhoI digested M13mp19.7 to form pDBD2 (Figure 4).

Linker 4

		M	K	W	V	S	F
5′	GATCC	ATG	AAG	TGG	GTA	AGC	TTT
	G	TAC	TTC	ACC	CAT	TCG	AAA

I	S	L	L	F	L	F	S
ATT	TCC	CTT	CTT	TTT	CTC	TTT	AGC
TAA	AGG	GAA	GAA	AAA	GAG	AAA	TCG

S	A	Y	S	R	G	V	F
TCG	GCT	TAT	TCC	AGG	GGT	GTG	TTT
AGC	CGA	ATA	AGG	TCC	CCA	CAC	AAA

R	R
CG	3′
GCAGCT	5′

In this linker the codon for the fourth amino acid after the initial methionine, ACC for threonine in the HSA pre-pro leader sequence (Lawn et al, 1981), has been changed to AGC for serine to create a HindIII site.

A sequence of synthetic DNA representing a part of the known HSA coding sequence (Lawn et al., 1981) (amino acids 382 to 387, Fig. 2), fused to part of the known fibronectin coding sequence (Kornblihtt et al., 1985) (amino acids 585 to 640, Fig. 2), was prepared by synthesising six oligonucleotides (Linker 5, Fig. 6). The oligonucleotides 2, 3, 4, 6, 7 and 8 were phosphorylated using T4 polynucleotide kinase and then the oligonucleotides were annealed under standard conditions in pairs, i.e. 1+8, 2+7, 3+6 and 4+5. The annealed oligonucleotides were then mixed together and ligated with mHOB12 which had previously been digested with the restriction enzymes HincII and EcoRI. The ligation mixture was then used to transfect E.coli XL1-Blue (Stratagene Cloning Systems, San Diego, CA). Single stranded template DNA was then prepared from mature bacteriophage particles derived from several independent plaques and then was analysed by DNA sequencing. A clone in which a linker of the expected sequence had been correctly inserted into the vector was designated pDBDF1 (Fig. 7). This plasmid was then digested with PstI and EcoRI and the approx. 0.24kb fragment was purified and then ligated with the 1.29kb BamHI-PstI fragment of pDBD2 (Fig. 7) and BamHI + EcoRI digested pUC19 (Yanisch-Perron, et al., 1985) to form pDBDF2 (Fig. 7).

A plasmid containing a DNA sequence encoding full length human fibronectin, pFHDEL1, was digested with EcoRI and XhoI and a 0.77kb EcoRI-xhoI fragment (Fig. 8) was isolated and then ligated with EcoRI and SalI digested M13 mp18 (Norrander et al., 1983) to form pDBDF3 (Fig. 8).

The following oligonucleotide linker (Linker 6) was synthesised, representing from the PstI site at 4784-4791 of the fibronectin sequence of EP-A-207 751 to the codon for tyrosine 1578 (Fig. 5) which is followed by a stop codon (TAA), a HindIII site and then a BamHI cohesive end:

Linker 6

```
                G     P     D     Q     T     E     M     T     I     E     G     L
               GGT   CCA   GAT   CAA   ACA   GAA   ATG   ACT   ATT   GAA   GGC   TTG
      A  CGT   CCA   GGT   CTA   GTT   TGT   CTT   TAC   TGA   TAA   CTT   CCG   AAC

      Q     P     T     V     E     Y          Stop
     CAG   CCC   ACA   GTG   GAG   TAT          TAA    GCTTG
     GTC   GGG   TGT   CAC   CTC   ATA          ATT    CGAACCTAG
```

This linker was then ligated with PstI and HindIII digested pDBDF3 to form pDBDF4 (Fig. 8). The following DNA fragments were then ligated together with BglII digested pKV50 (EP-A-258 067) as shown in Fig. 8: 0.68kb EcoRI-BamHI fragment of pDBDF4, 1.5kb BamHI-StuI fragment of pDBDF2 and the 2.2kb StuI-EcoRI fragment of pFHDEL1. The resultant plasmid pDBDF5 (Fig. 8) includes the promoter of EP-A-258 067 to direct the expression of the HSA secretion signal fused to DNA encoding amino acids 1-387 of mature HSA, in turn fused directly and in frame with DNA encoding amino acids 585-1578 of human fibronectin, after which translation would terminate at the stop codon TAA. This is then followed by the S.cerevisiae PGK gene transcription terminator. The plasmid also contains sequences which permit selection and maintenance in Escherichia coli and S.cerevisiae (EP-A-258 067).

This plasmid was introduced into S.cerevisiae S150-2B (leu2-3 leu2-112 ura3-52 trpl-289 his3- 1) by standard procedures (Beggs, 1978). Transformants were subsequently analysed and found to produce the HSA-fibronectin fusion protein.

EXAMPLE 2 : HSA 1-195 FUSED TO Fn 585-1578

In this second example the first domain of human serum albumin (amino acids 1-195) is fused to amino acids 585-1578 of human fibronectin.

The plasmid pDBD2 was digested with BamHI and BglII and the 0.79kb fragment was purified and then ligated with BamHI-digested M13mp19 to form pDBDF6 (Fig. 6). The following oligonucleotide:

5′-C C A A A G C T C G A G G A A C T T C G-3′

was used as a mutagenic primer to create a XhoI site in pDBDF6 by in vitro mutagenesis using a kit supplied by Amersham International PLC. This site was created by changing base number 696 of HSA from a T to a G (Fig. 2). The plasmid thus formed was designated pDBDF7 (Fig. 9). The following linker was then synthesised to represent from this newly created XhoI site to the codon for lysine 195 of HSA (AAA) and then from the codon for isoleucine 585 of fibronectin to the ends of oligonucleotides 1 and 8 shown in Fig. 6.

Linker 7

```
    D   E   L   R   D   E   G   K   A   S   S   A   K
TC GAT GAA CTT CGG GAT GAA GGG AAG GCT TCG TCT GCC AAA
    A CTT GAA GCC CTA CTT CCC TTC CGA AGC AGA CGG TTT

    I   T   E   T   P   S   Q   P   N   S   H
   ATC ACT GAG ACT CCG AGT CAG C
   TAG TGA CTC TGA GGC TCA GTC GGG TTG AGG GTG G
```

This linker was ligated with the annealed oligonucleotides shown in Fig. 3, i.e. 2+7, 3+6 and 4+5 together with XhoI and EcoRI digested pDBDF7 to form pDBDF8 (Fig. 9). Note that in order to recreate the original HSA DNA sequence, and hence amino acid sequence, insertion of linker 7 and the other oligonucleotides into pDBDF7 does not recreate the XhoI site.

The 0.83kb BamHi-StuI fragment of pDBDF8 was purified and then was ligated with the 0.68kb EcoRI-BamHI fragment of pDBDF2 and the 2.22kb StuI-EcoRI fragment of pFHDEL1 into BglII-digested pKV50 to form pDBDF9 (Fig. 9). This plasmid is similar to pDBDF5 except that it specifies only residues 1-195 of HSA rather than 1-387 as in pDBDF5.

When introduced into S.cerevisiae S150-2B as above, the plasmid directed the expression and secretion of a hybrid molecule composed of residues 1-195 of HSA fused to residues 585-1578 of fibronectin.

EXAMPLE 3 : HSA 1-387 FUSED TO Fn 585-1578, AS CLEAVABLE MOLECULE

In order to facilitate production of large amounts of residues 585-1578 of fibronectin, a construct was made in which DNA encoding residues 1-387 of HSA was separated from DNA encoding residues 585-1578 of fibronectin by the sequence

```
 I   E   G   R
ATT GAA GGT AGA
TAA CTT CCA TCT
```

which specifies the cleavage recognition site for the blood clotting Factor X. Consequently the purified secreted product can be treated with Factor X and then the fibronectin part of the molecule can be separated from the HSA part.

To do this two oligonucleotides were synthesised and then annealed to form Linker 8.

Linker 8

E	E	P	Q	N	L	I	E	G
GAA	GAG	CCT	CAG	AAT	TTA	ATT	GAA	GGT
CTT	CTC	GGA	GTC	TTA	AAT	TAA	CTT	CCA
R	I	T	E	T	P	S	Q	P
AGA	ATC	ACT	GAG	ACT	CCG	AGT	CAG	C
TCT	TAG	TGA	CTC	TGA	GGC	TCA	GTC	GGG
N	S	H						
TTG	AGG	GTG G						

This linker was then ligated with the annealed oligonucleotides shown in Fig. 6, i.e. 2+7, 3+6 and 4+5 into HincII andEcoRI digested mHOB12, to form pDBDF10 (Fig. 7). The plasmid was then digested with PstI and EcoRI and the roughly 0.24kb fragment was purified and then ligated with the 1.29kb BamHi-PstI fragment of pDBD2 and BamHi and EcoRI digested pUC19 to form pDBDF11 (Fig. 10).

The 1.5kb BamHi-StuI fragment of pDBDF11 was then ligated with the 0.68kb EcoRI-BamH1 fragment of pDBDF4 and the 2.22kb StuI-EcoRI fragment of pFHDEL1 into BglII-digested pKV50 to form pDBDF12 (Fig. 10). This plasmid was then introduced into S.cerevisiae S150-2B. The purified secreted fusion protein was treated with Factor X to liberate the fibronectin fragment representing residues 585-1578 of the native molecule.

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Claims

1. A fusion polypeptide comprising, as at least part of the N-terminal portion thereof, an N-terminal portion of HSA or a variant thereof and, as at least part of the C-terminal portion thereof, another polypeptide except that, when the said N-terminal portion of HSA is the 1-n portion where n is 369 to 419 or a variant thereof then the said polypeptide is (a) the 585 to 1578 portion of human fibronectin or a variant thereof, (b) the 1 to 368 portion of CD4 or a variant thereof, (c) platelet derived growth factor or a variant thereof, (d) transforming growth factor β or a variant thereof, (e) the 1-261 portion of mature human plasma fibronectin or a variant thereof, (f) the 278-578 portion of mature human plasma fibronectin or a variant

thereof, (g) the 1-272 portion of mature human von Willebrand's Factor or a variant thereof, or (h) alpha-1-antitrypsin or a variant thereof.

2. A fusion polypeptide according to Claim 1 additionally comprising at least one N-terminal amino acid extending beyond the portion corresponding to the N-terminal portion of HSA.

3. A fusion polypeptide according to Claim 1 or 2 wherein there is a cleavable region at the junction of the said N-terminal or C-terminal portions.

4. A fusion polypeptide according to any one of the preceding claims wherein the said C-terminal portion is the 585 to 1578 portion of human plasma fibronectin or a variant thereof.

5. A transformed or transfected host having a nucleotide sequence so arranged as to express a fusion polypeptide according to any one of the preceding claims.

6. A process for preparing a fusion polypeptide by cultivation of a host according to Claim 5, followed by separation of the fusion polypeptide in a useful form.

7. A fusion polypeptide according to any one of Claims 1 to 4 for use in therapy.

FIGURE 1

10 20
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys

30 40
Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val

50 60
Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu

70 80
Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

90 100
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu

110 120
Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val

130 140
Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr

150 160
Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

170 180
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro

190 200
Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys

210 220
Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser

230 240
Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys

250 260
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu

270 280
Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu

290 300
Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala

310 320
Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

330 340
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp

350 360
Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys

370 380
Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu

FIGURE 1 Cont.

390 400
Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

410 420
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr

430 440
Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His

450 460
Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu

470 480
Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

490 500
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys

510 520
Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu

530 540
Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr

550 560
Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

570 580
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln

Ala Ala Leu Gly Leu

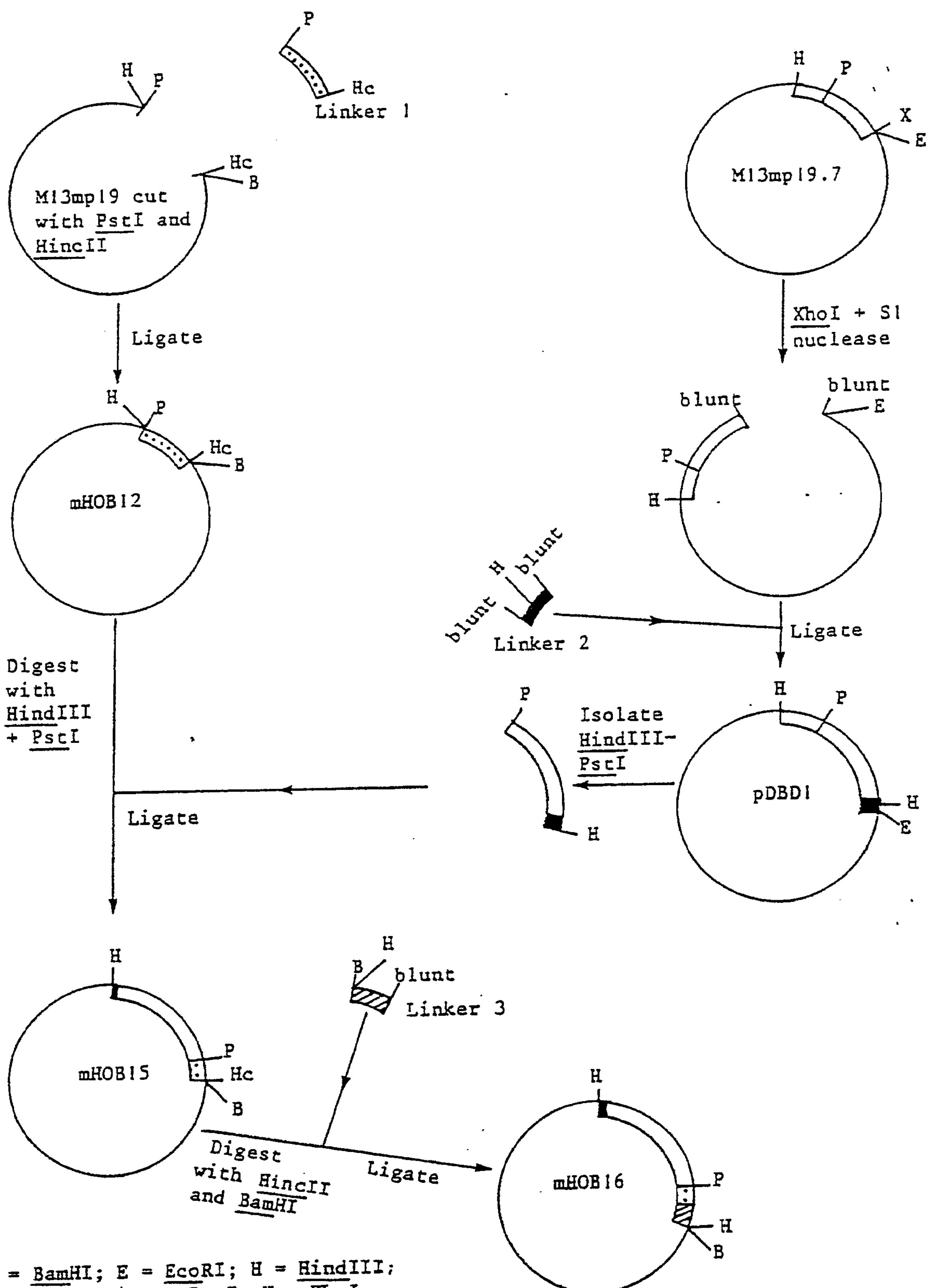
FIGURE 2 DNA sequence coding for mature HSA

```
        10        20        30        40        50        60        70        80
GATGCACACAAGAGTGAGGTTGCTCATCGGTTTAAAGATTTGGGAGAAGAAAATTTCAAAGCCTTGGTGTTGATTGCCTT
 D  A  H  K  S  E  V  A  H  R  F  K  D  L  G  E  E  N  F  K  A  L  V  L  I  A  F

        90       100       110       120       130       140       150       160
TGCTCAGTATCTTCAGCAGTGTCCATTTGAAGATCATGTAAAATTAGTGAATGAAGTAACTGAATTTGCAAAAACATGTG
  A  Q  Y  L  Q  Q  C  P  F  E  D  H  V  K  L  V  N  E  V  T  E  F  A  K  T  C

       170       180       190       200       210       220       230       240
TTGCTGATGAGTCAGCTGAAAATTGTGACAAATCACTTCATACCCTTTTTGGAGACAAATTATGCACAGTTGCAACTCTT
V  A  D  E  S  A  E  N  C  D  K  S  L  H  T  L  F  G  D  K  L  C  T  V  A  T  L

       250       260       270       280       290       300       310       320
CGTGAAACCTATGGTGAAATGGCTGACTGCTGTGCAAAACAAGAACCTGAGAGAAATGAATGCTTCTTGCAACACAAAGA
 R  E  T  Y  G  E  M  A  D  C  C  A  K  Q  E  P  E  R  N  E  C  F  L  Q  H  K  D

       330       340       350       360       370       380       390       400
TGACAACCCAAACCTCCCCCGATTGGTGAGACCAGAGGTTGATGTGATGTGCACTGCTTTTCATGACAATGAAGAGACAT
  D  N  P  N  L  P  R  L  V  R  P  E  V  D  V  M  C  T  A  F  H  D  N  E  E  T

       410       420       430       440       450       460       470       480
TTTTGAAAAAATACTTATATGAAATTGCCAGAAGACATCCTTACTTTTATGCCCCGGAACTCCTTTTCTTTGCTAAAAGG
F  L  K  K  Y  L  Y  E  I  A  R  R  H  P  Y  F  Y  A  P  E  L  L  F  F  A  K  R

       490       500       510       520       530       540       550       560
TATAAAGCTGCTTTTACAGAATGTTGCCAAGCTGCTGATAAAGCTGCCTGCCTGTTGCCAAAGCTCGATGAACTTCGGGA
 Y  K  A  A  F  T  E  C  C  Q  A  A  D  K  A  A  C  L  L  P  K  L  D  E  L  R  D

       570       580       590       600       610       620       630       640
TGAAGGGAAGGCTTCGTCTGCCAAACAGAGACTCAAATGTGCCAGTCTCCAAAAATTTGGAGAAAGAGCTTTCAAAGCAT
  E  G  K  A  S  S  A  K  Q  R  L  K  C  A  S  L  Q  K  F  G  E  R  A  F  K  A

       650       660       670       680       690       700       710       720
GGGCAGTGGCTCGCCTGAGCCAGAGATTTCCCAAAGCTGAGTTTGCAGAAGTTTCCAAGTTAGTGACAGATCTTACCAAA
W  A  V  A  R  L  S  Q  R  F  P  K  A  E  F  A  E  V  S  K  L  V  T  D  L  T  K

       730       740       750       760       770       780       790       800
GTCCACACGGAATGCTGCCATGGAGATCTGCTTGAATGTGCTGATGACAGGGCGGACCTTGCCAAGTATATCTGTGAAAA
 V  H  T  E  C  C  H  G  D  L  L  E  C  A  D  D  R  A  D  L  A  K  Y  I  C  E  N

       810       820       830       840       850       860       870       880
TCAGGATTCGATCTCCAGTAAACTGAAGGAATGCTGTGAAAAACCTCTGTTGGAAAAATCCCACTGCATTGCCGAAGTGG
  Q  D  S  I  S  S  K  L  K  E  C  C  E  K  P  L  L  E  K  S  H  C  I  A  E  V

       890       900       910       920       930       940       950       960
AAAATGATGAGATGCCTGCTGACTTGCCTTCATTAGCTGCTGATTTTGTTGAAAGTAAGGATGTTTGCAAAAACTATGCT
E  N  D  E  M  P  A  D  L  P  S  L  A  A  D  F  V  E  S  K  D  V  C  K  N  Y  A

       970       980       990      1000      1010      1020      1030      1040
GAGGCAAAGGATGTCTTCCTGGGCATGTTTTTGTATGAATATGCAAGAAGGCATCCTGATTACTCTGTCGTGCTGCTGCT
 E  A  K  D  V  F  L  G  M  F  L  Y  E  Y  A  R  R  H  P  D  Y  S  V  V  L  L  L
```

FIGURE 2 Cont.

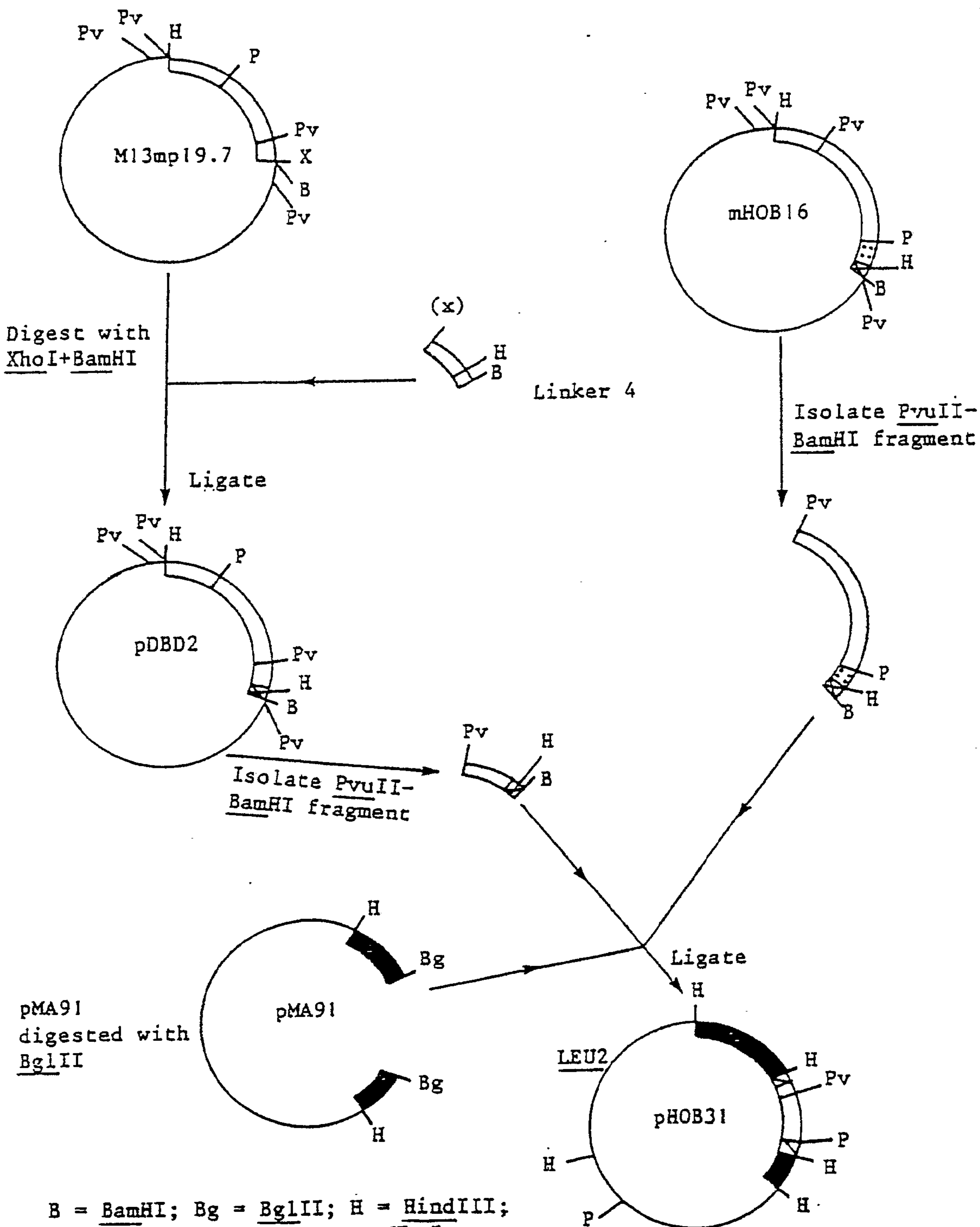
```
      1050      1060      1070      1080      1090      1100      1110      1120
GAGACTTGCCAAGACATATGAAACCACTCTAGAGAAGTGCTGTGCCGCTGCAGATCCTCATGAATGCTATGCCAAAGTGT
 R  L  A  K  T  Y  E  T  T  L  E  K  C  C  A  A  A  D  P  H  E  C  Y  A  K  V

      1130      1140      1150      1160      1170      1180      1190      1200
TCGATGAATTTAAACCTCTTGTGGAAGAGCCTCAGAATTTAATCAAACAAAACTGTGAGCTTTTTGAGCAGCTTGGAGAG
F  D  E  F  K  P  L  V  E  E  P  Q  N  L  I  K  Q  N  C  E  L  F  E  Q  L  G  E

      1210      1220      1230      1240      1250      1260      1270      1280
TACAAATTCCAGAATGCGCTATTAGTTCGTTACACCAAGAAAGTACCCCAAGTGTCAACTCCAACTCTTGTAGAGGTCTC
 Y  K  F  Q  N  A  L  L  V  R  Y  T  K  K  V  P  Q  V  S  T  P  T  L  V  E  V  S

      1290      1300      1310      1320      1330      1340      1350      1360
AAGAAACCTAGGAAAAGTGGGCAGCAAATGTTGTAAACATCCTGAAGCAAAAAGAATGCCCTGTGCAGAAGACTATCTAT
 R  N  L  G  K  V  G  S  K  C  C  K  H  P  E  A  K  R  M  P  C  A  E  D  Y  L

      1370      1380      1390      1400      1410      1420      1430      1440
CCGTGGTCCTGAACCAGTTATGTGTGTTGCATGAGAAAACGCCAGTAAGTGACAGAGTCACAAAATGCTGCACAGAGTCC
S  V  V  L  N  Q  L  C  V  L  H  E  K  T  P  V  S  D  R  V  T  K  C  C  T  E  S

      1450      1460      1470      1480      1490      1500      1510      1520
TTGGTGAACAGGCGACCATGCTTTTCAGCTCTGGAAGTCGATGAAACATACGTTCCCAAAGAGTTTAATGCTGAAACATT
 L  V  N  R  R  P  C  F  S  A  L  E  V  D  E  T  Y  V  P  K  E  F  N  A  E  T  F

      1530      1540      1550      1560      1570      1580      1590      1600
CACCTTCCATGCAGATATATGCACACTTTCTGAGAAGGAGAGACAAATCAAGAAACAAACTGCACTTGTTGAGCTTGTGA
 T  F  H  A  D  I  C  T  L  S  E  K  E  R  Q  I  K  K  Q  T  A  L  V  E  L  V

      1610      1620      1630      1640      1650      1660      1670      1680
AACACAAGCCCAAGGCAACAAAAGAGCAACTGAAAGCTGTTATGGATGATTTCGCAGCTTTTGTAGAGAAGTGCTGCAAG
K  H  K  P  K  A  T  K  E  Q  L  K  A  V  M  D  D  F  A  A  F  V  E  K  C  C  K

      1690      1700      1710      1720      1730      1740      1750      1760
GCTGACGATAAGGAGACCTGCTTTGCCGAGGAGGGTAAAAAACTTGTTGCTGCAAGTCAAGCTGCCTTAGGCTTATAACA
 A  D  D  K  E  T  C  F  A  E  E  G  K  K  L  V  A  A  S  Q  A  A  L  G  L

      1770      1780
TCTACATTTAAAAGCATCTCAG
```

FIGURE 3 Construction of mHOB16



B = BamHI; E = EcoRI; H = HindIII;
Hc = HincII; P = PstI; X = XhoI

FIGURE 4 Construction of pHOB31



B = BamHI; Bg = BglII; H = HindIII;
P = PstI; Pv = PvuII; X = XhoI

									10										20
Gln	Ala	Gln	Gln	Met	Val	Gln	Pro	Gln	Ser	Pro	Val	Ala	Val	Ser	Gln	Ser	Lys	Pro	Gly
									30										40
Cys	Tyr	Asp	Asn	Gly	Lys	His	Tyr	Gln	Ile	Asn	Gln	Gln	Trp	Glu	Arg	Thr	Tyr	Leu	Gly
									50										60
Asn	Val	Leu	Val	Cys	Thr	Cys	Tyr	Gly	Gly	Ser	Arg	Gly	Phe	Asn	Cys	Glu	Ser	Lys	Pro
									70										80
Glu	Ala	Glu	Glu	Thr	Cys	Phe	Asp	Lys	Tyr	Thr	Gly	Asn	Thr	Tyr	Arg	Val	Gly	Asp	Thr
									90										100
Tyr	Glu	Arg	Pro	Lys	Asp	Ser	Met	Ile	Trp	Asp	Cys	Thr	Cys	Ile	Gly	Ala	Gly	Arg	Gly
									110										120
Arg	Ile	Ser	Cys	Thr	Ile	Ala	Asn	Arg	Cys	His	Glu	Gly	Gly	Gln	Ser	Tyr	Lys	Ile	Gly
									130										140
Asp	Thr	Trp	Arg	Arg	Pro	His	Glu	Thr	Gly	Gly	Tyr	Met	Leu	Glu	Cys	Val	Cys	Leu	Gly
									150										160
Asn	Gly	Lys	Gly	Glu	Trp	Thr	Cys	Lys	Pro	Ile	Ala	Glu	Lys	Cys	Phe	Asp	His	Ala	Ala
									170										180
Gly	Thr	Ser	Tyr	Val	Val	Gly	Glu	Thr	Trp	Glu	Lys	Pro	Tyr	Gln	Gly	Trp	Met	Met	Val
									190										200
Asp	Cys	Thr	Cys	Leu	Gly	Glu	Gly	Ser	Gly	Arg	Ile	Thr	Cys	Thr	Ser	Arg	Asn	Arg	Cys
									210										220
Asn	Asp	Gln	Asp	Thr	Arg	Thr	Ser	Tyr	Arg	Ile	Gly	Asp	Thr	Trp	Ser	Lys	Lys	Asp	Asn
									230										240
Arg	Gly	Asn	Leu	Leu	Gln	Cys	Ile	Cys	Thr	Gly	Asn	Gly	Arg	Gly	Glu	Trp	Lys	Cys	Glu
									250										260
Arg	His	Thr	Ser	Val	Gln	Thr	Thr	Ser	Ser	Gly	Ser	Gly	Pro	Phe	Thr	Asp	Val	Arg	Ala
									270										280
Ala	Val	Tyr	Gln	Pro	Gln	Pro	His	Pro	Gln	Pro	Pro	Pro	Tyr	Gly	His	Cys	Val	Thr	Asp
									290										300
Ser	Gly	Val	Val	Tyr	Ser	Val	Gly	Met	Gln	Trp	Leu	Lys	Thr	Gln	Gly	Asn	Lys	Gln	Met
									310										320
Leu	Cys	Thr	Cys	Leu	Gly	Asn	Gly	Val	Ser	Cys	Gln	Glu	Thr	Ala	Val	Thr	Gln	Thr	Tyr
									330										340
Gly	Gly	Asn	Ser	Asn	Gly	Glu	Pro	Cys	Val	Leu	Pro	Phe	Thr	Tyr	Asn	Gly	Arg	Thr	Phe
									350										360
Tyr	Ser	Cys	Thr	Thr	Glu	Gly	Arg	Gln	Asp	Gly	His	Leu	Trp	Cys	Ser	Thr	Thr	Ser	Asn
									370										380
Tyr	Glu	Gln	Asp	Gln	Lys	Tyr	Ser	Phe	Cys	Thr	Asp	His	Thr	Val	Leu	Val	Gln	Thr	Gln
									390										400
Gly	Gly	Asn	Ser	Asn	Gly	Ala	Leu	Cys	His	Phe	Pro	Phe	Leu	Tyr	Asn	Asn	His	Asn	Tyr
									410										420
Thr	Asp	Cys	Thr	Ser	Glu	Gly	Arg	Arg	Asp	Asn	Met	Lys	Trp	Cys	Gly	Thr	Thr	Gln	Asn

FIGURE 5A

FNDEL1

```
                                             430                                               440
Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met Ala Ala His Glu Glu Ile Cys Thr
                                             450                                               460
Thr Asn Glu Gly Val Met Tyr Arg Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly
                                             470                                               480
His Met Met Arg Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Tyr Ala Tyr
                                             490                                               500
Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val Asn Asp Thr Phe
                                             510                                               520
His Lys Arg His Glu Glu Gly His Met Leu Asn Cys Thr Cys Phe Gly Gln Gly Arg Gly
                                             530                                               540
Arg Trp Lys Cys Asp Pro Val Asp Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln
                                             550                                               560
Ile Gly Asp Ser Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly
                                             570                                               580
Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser Ser Ser Gly Pro
                                             590                                               600
Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro Asn Ser His Pro Ile Gln Trp Asn
                                             610                                               620
Ala Pro Gln Pro Ser His Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val
                                             630                                               640
Gly Arg Trp Lys Glu Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu
                                             650                                               660
Lys Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr Gly His Gln Glu
                                             670                                               680
Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser Thr Pro Val Thr Ser Asn Thr Val
                                             690                                               700
Thr Gly Glu Thr Thr Pro Phe Ser Pro Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile
                                             710                                               720
Thr Ala Ser Ser Phe Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg
                                             730                                               740
Val Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp Leu Pro Ser Thr
                                             750                                               760
Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly Arg Lys Tyr Ile Val Asn Val Tyr
                                             770                                               780
Gln Ile Ser Glu Asp Gly Glu Gln Ser Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro
                                             790                                               800
Asp Ala Pro Pro Asp Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val Val Arg Trp
                                             810                                               820
Ser Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val Tyr Ser Pro Ser Val Glu Gly
                                             830                                               840
Ser Ser Thr Glu Leu Asn Leu Pro Glu Thr Ala Asn Ser Val Thr Leu Ser Asp Leu Gln
```

FNDEL1

FIGURE 5B

									850										860
Pro	Gly	Val	Gln	Tyr	Asn	Ile	Thr	Ile	Tyr	Ala	Val	Glu	Glu	Asn	Gln	Glu	Ser	Thr	Pro
									870										880
Val	Val	Ile	Gln	Gln	Glu	Thr	Thr	Gly	Thr	Pro	Arg	Ser	Asp	Thr	Val	Pro	Ser	Pro	Arg
									890										900
Asp	Leu	Gln	Phe	Val	Glu	Val	Thr	Asp	Val	Lys	Val	Thr	Ile	Met	Trp	Thr	Pro	Pro	Glu
									910										920
Ser	Ala	Val	Thr	Gly	Tyr	Arg	Val	Asp	Val	Ile	Pro	Val	Asn	Leu	Pro	Gly	Glu	His	Gly
									930										940
Gln	Arg	Leu	Pro	Ile	Ser	Arg	Asn	Thr	Phe	Ala	Glu	Val	Thr	Gly	Leu	Ser	Pro	Gly	Val
									950										960
Thr	Tyr	Tyr	Phe	Lys	Val	Phe	Ala	Val	Ser	His	Gly	Arg	Glu	Ser	Lys	Pro	Leu	Thr	Ala
									970										980
Gln	Gln	Thr	Thr	Lys	Leu	Asp	Ala	Pro	Thr	Asn	Leu	Gln	Phe	Val	Asn	Glu	Thr	Asp	Ser
									990										1000
Thr	Val	Leu	Val	Arg	Trp	Thr	Pro	Pro	Arg	Ala	Gln	Ile	Thr	Gly	Tyr	Arg	Leu	Thr	Val
									1010										1020
Gly	Leu	Thr	Arg	Arg	Gly	Gln	Pro	Arg	Gln	Tyr	Asn	Val	Gly	Pro	Ser	Val	Ser	Lys	Tyr
									1030										1040
Pro	Leu	Arg	Asn	Leu	Gln	Pro	Ala	Ser	Glu	Tyr	Thr	Val	Ser	Leu	Val	Ala	Ile	Lys	Gly
									1050										1060
Asn	Gln	Glu	Ser	Pro	Lys	Ala	Thr	Gly	Val	Phe	Thr	Thr	Leu	Gln	Pro	Gly	Ser	Ser	Ile
									1070										1080
Pro	Pro	Tyr	Asn	Thr	Glu	Val	Thr	Glu	Thr	Thr	Ile	Val	Ile	Thr	Trp	Thr	Pro	Ala	Pro
									1090										1100
Arg	Ile	Gly	Phe	Lys	Leu	Gly	Val	Arg	Pro	Ser	Gln	Gly	Gly	Glu	Ala	Pro	Arg	Glu	Val
									1110										1120
Thr	Ser	Asp	Ser	Gly	Ser	Ile	Val	Val	Ser	Gly	Leu	Thr	Pro	Gly	Val	Glu	Tyr	Val	Tyr
									1130										1140
Thr	Ile	Gln	Val	Leu	Arg	Asp	Gly	Gln	Glu	Arg	Asp	Ala	Pro	Ile	Val	Asn	Lys	Val	Val
									1150										1160
Thr	Pro	Leu	Ser	Pro	Pro	Thr	Asn	Leu	His	Leu	Glu	Ala	Asn	Pro	Asp	Thr	Gly	Val	Leu
									1170										1180
Thr	Val	Ser	Trp	Glu	Arg	Ser	Thr	Thr	Pro	Asp	Ile	Thr	Gly	Tyr	Arg	Ile	Thr	Thr	Thr
									1190										1200
Pro	Thr	Asn	Gly	Gln	Gln	Gly	Asn	Ser	Leu	Glu	Glu	Val	Val	His	Ala	Asp	Gln	Ser	Ser
									1210										1220
Cys	Thr	Phe	Asp	Asn	Leu	Ser	Pro	Gly	Leu	Glu	Tyr	Asn	Val	Ser	Val	Tyr	Thr	Val	Lys
									1230										1240
Asp	Asp	Lys	Glu	Ser	Val	Pro	Ile	Ser	Asp	Thr	Ile	Ile	Pro	Ala	Val	Pro	Pro	Pro	Thr
									1250										1260
Asp	Leu	Arg	Phe	Thr	Asn	Ile	Gly	Pro	Asp	Thr	Met	Arg	Val	Thr	Trp	Ala	Pro	Pro	Pro

FIGURE 5C

FNDEL1

1270 1280
Ser Ile Asp Leu Thr Asn Phe Leu Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val

1290 1300
Ala Glu ~~Leu Ser~~ Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu Pro Gly

1310 1320
Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln His Glu Ser Thr Pro Leu Arg

1330 1340
Gly Arg Gln Lys Thr Gly Leu Asp Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala

1350 1360
Asn Ser Phe Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg Ile Arg

1370 1380
His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp Arg Val Pro His Ser Arg Asn

1390 1400
Ser Ile Thr Leu Thr Asn Leu Thr Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu

1410 1420
Asn Gly Arg Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp Val Pro

1430 1440
Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro

1450 1460
Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val

1470 1480
Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly

1490 1500
Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser

1510 1520
Lys Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln Met Gln Val Thr

1530 1540
Asp Val Gln Asp Asn Ser Ile Ser Val Lys Trp Leu Pro Ser Ser Ser Pro Val Thr Gly

1550 1560
Tyr Arg Val Thr Thr Thr Pro Lys Asn Gly Pro Gly Pro Thr Lys Thr Lys Thr Ala Gly

1570 1580
Pro Asp Gln Thr Glu Met Thr Ile Glu Gly Leu Gln Pro Thr Val Glu Tyr Val Val Ser

1590 1600
Val Tyr Ala Gln Asn Pro Ser Gly Glu Ser Gln Pro Leu Val Gln Thr Ala Val Thr Thr

1610 1620
Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln

1630 1640
Trp Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu Lys

1650 1660
Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser Gly

1670 1680
Leu Met Val Ala Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser

[illegible]

FIGURE 5D

1690 1700
Arg Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg

1710 1720
Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu Thr Ile

1730 1740
Thr Gly Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile

1750 1760
Lys Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile

1770 1780
Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser Thr

1790 1800
Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val

1810 1820
Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly

1830 1840
Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr

1850 1860
Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys

1870 1880
Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr Asp Glu Leu Pro Gln Leu Val Thr Leu Pro

1890 1900
His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro Ser Thr Val Gln Lys Thr Pro

1910 1920
Phe Val Thr His Pro Gly Tyr Asp Thr Gly Asn Gly Ile Gln Leu Pro Gly Thr Ser Gly

1930 1940
Gln Gln Pro Ser Val Gly Gln Gln Met Ile Phe Glu Glu His Gly Phe Arg Arg Thr Thr

1950 1960
Pro Pro Thr Thr Ala Thr Pro Ile Arg His Arg Pro Arg Pro Tyr Pro Pro Asn Val Ala

1970 1980
Leu Ser Gln Thr Thr Ile Ser Trp Ala Pro Phe Gln Asp Thr Ser Glu Tyr Ile Ile Ser

1990 2000
Cys His Pro Val Gly Thr Asp Glu Glu Pro Leu Gln Phe Arg Val Pro Gly Thr Ser Thr

2010 2020
Ser Ala Thr Leu Thr Gly Leu Thr Arg Gly Ala Thr Tyr Asn Ile Ile Val Glu Ala Leu

2030 2040
Lys Asp Gln Gln Arg His Lys Val Arg Glu Glu Val Val Thr Val Gly Asn Ser Val Asn

2050 2060
Glu Gly Leu Asn Gln Pro Thr Asp Asp Ser Cys Phe Asp Pro Tyr Thr Val Ser His Tyr

2070 2080
Ala Val Gly Asp Glu Trp Glu Arg Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys

2090 2100
Leu Gly Phe Gly Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys His Asp Asn Gly

FIGURE 5E

FNDEL1

```
                                             2110                                                  2120
Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln Gly Glu Asn Gly Gln Met Met Ser
                                             2130                                                  2140
Cys Thr Cys Leu Gly Asn Gly Lys Gly Glu Phe Lys Cys Asp Pro His Glu Ala Thr Cys
                                             2150                                                  2160
Tyr Asp Asp Gly Lys Thr Tyr His Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu Gly Ala
                                             2170                                                  2180
Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys Asp Asn Cys Arg Arg
                                             2190                                                  2200
Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr Gly Gln Ser Tyr Asn Gln Tyr Ser Gln
                                             2210                                                  2220
Arg Tyr His Gln Arg Thr Asn Thr Asn Val Asn Cys Pro Ile Glu Cys Phe Met Pro Leu
                                             2230
Asp Val Gln Ala Asp Arg Glu Asp Ser Arg Glu
```

FIGURE 5F

Figure 6. Linker 5 showing the eight constituent oligonucleotides

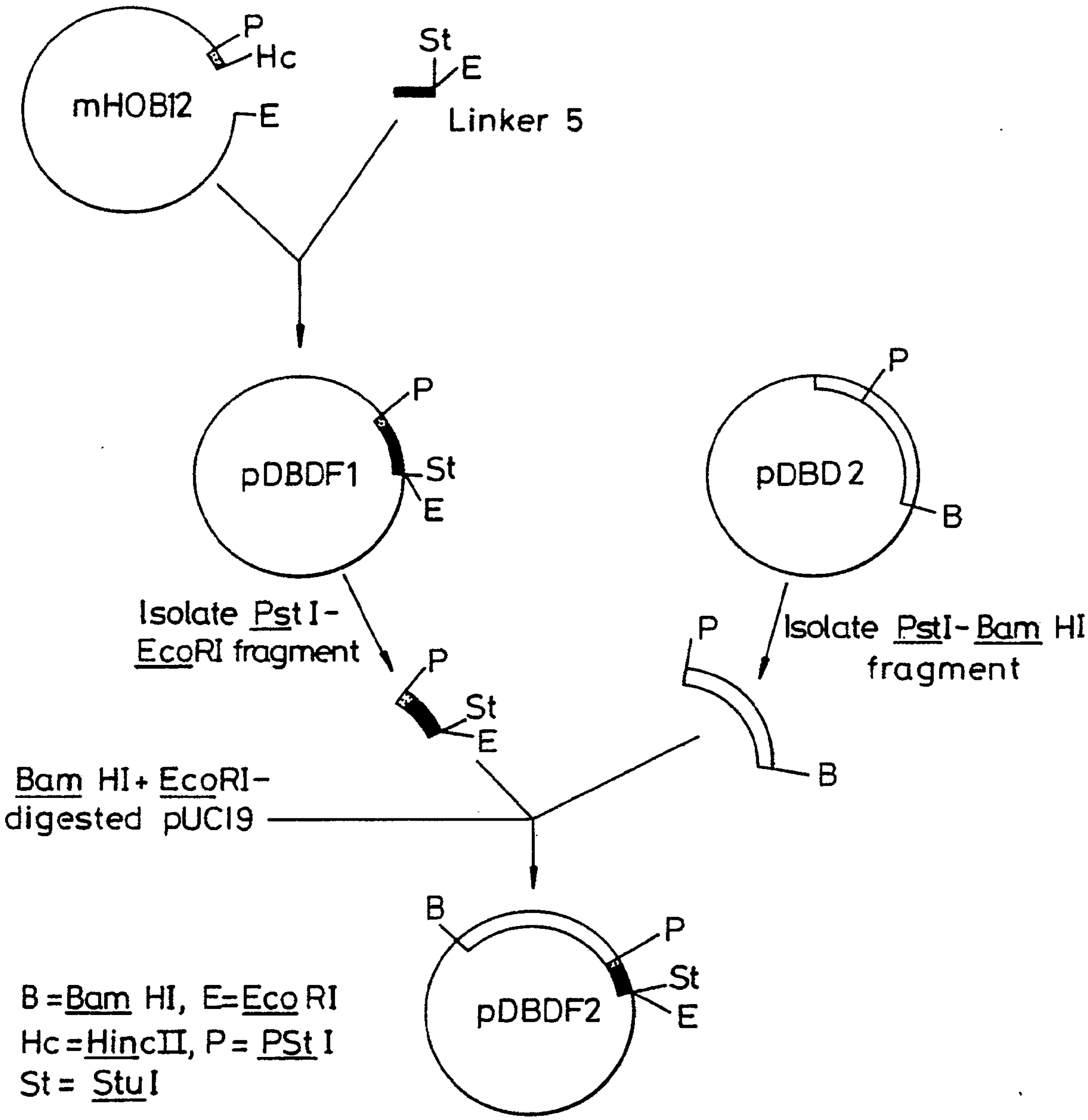


Fig. 7 Construction of pDBDF2

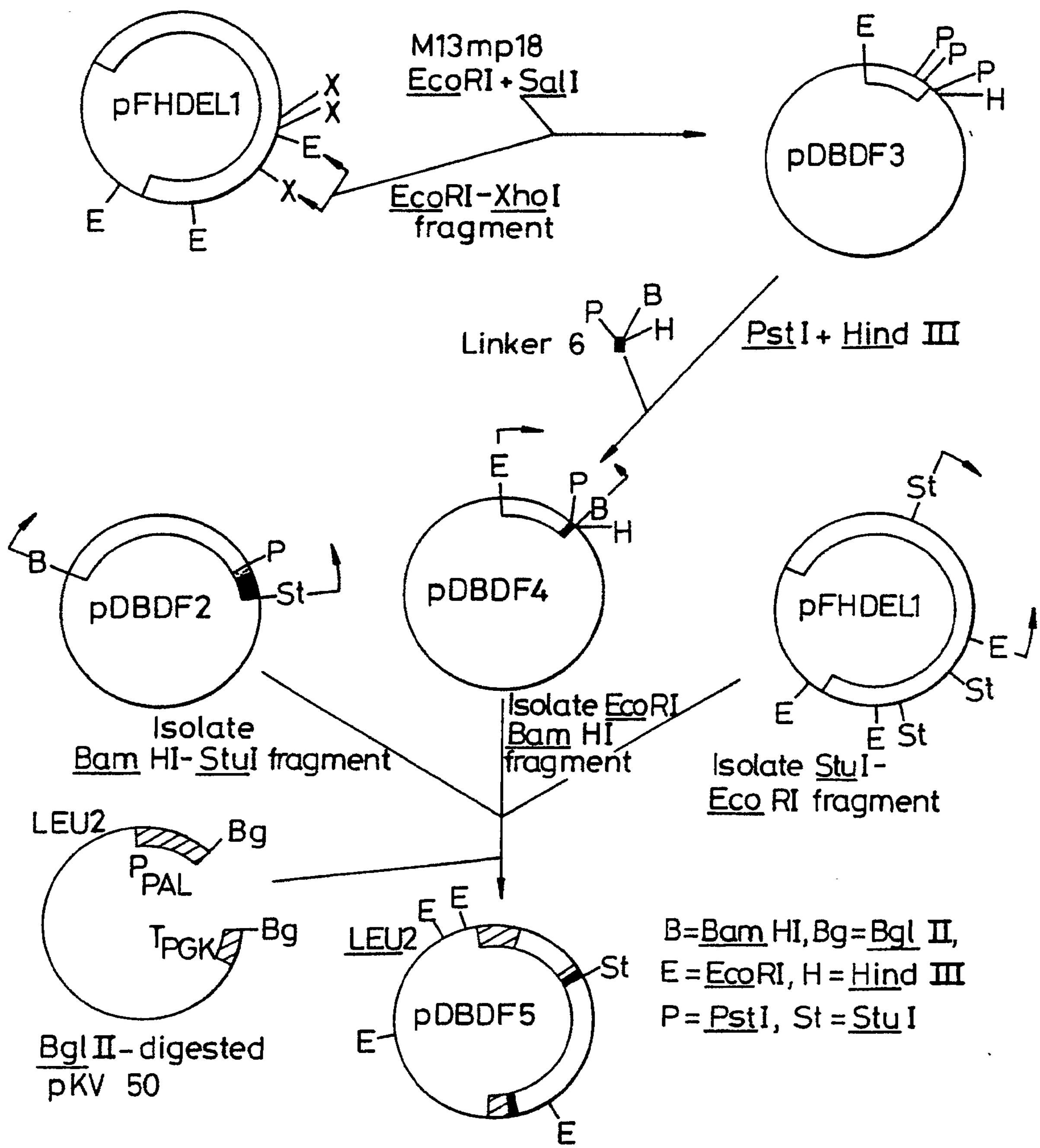


Fig. 8 Construction of pDBDF5

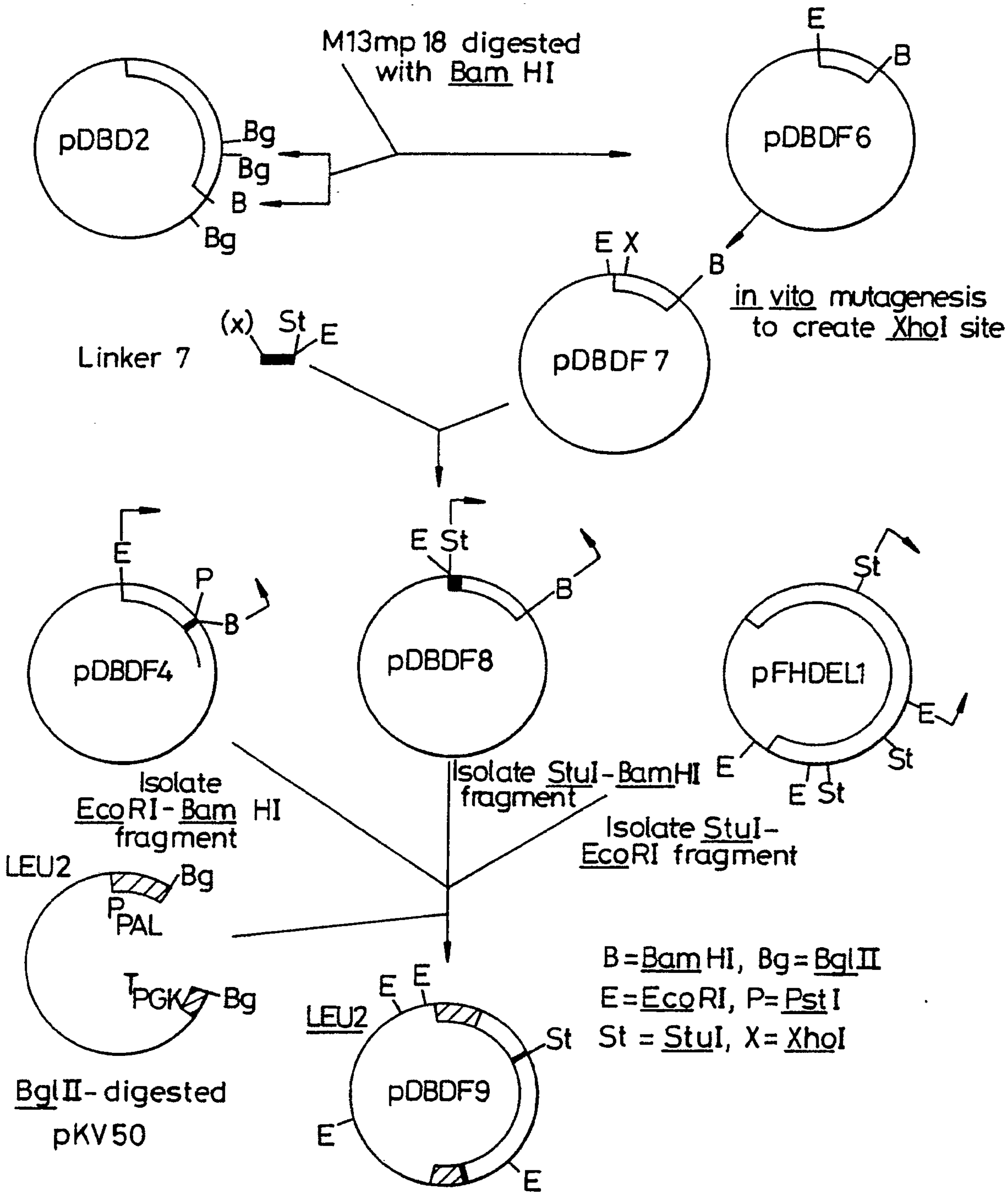


Fig. 9 Construction of pDBDF9

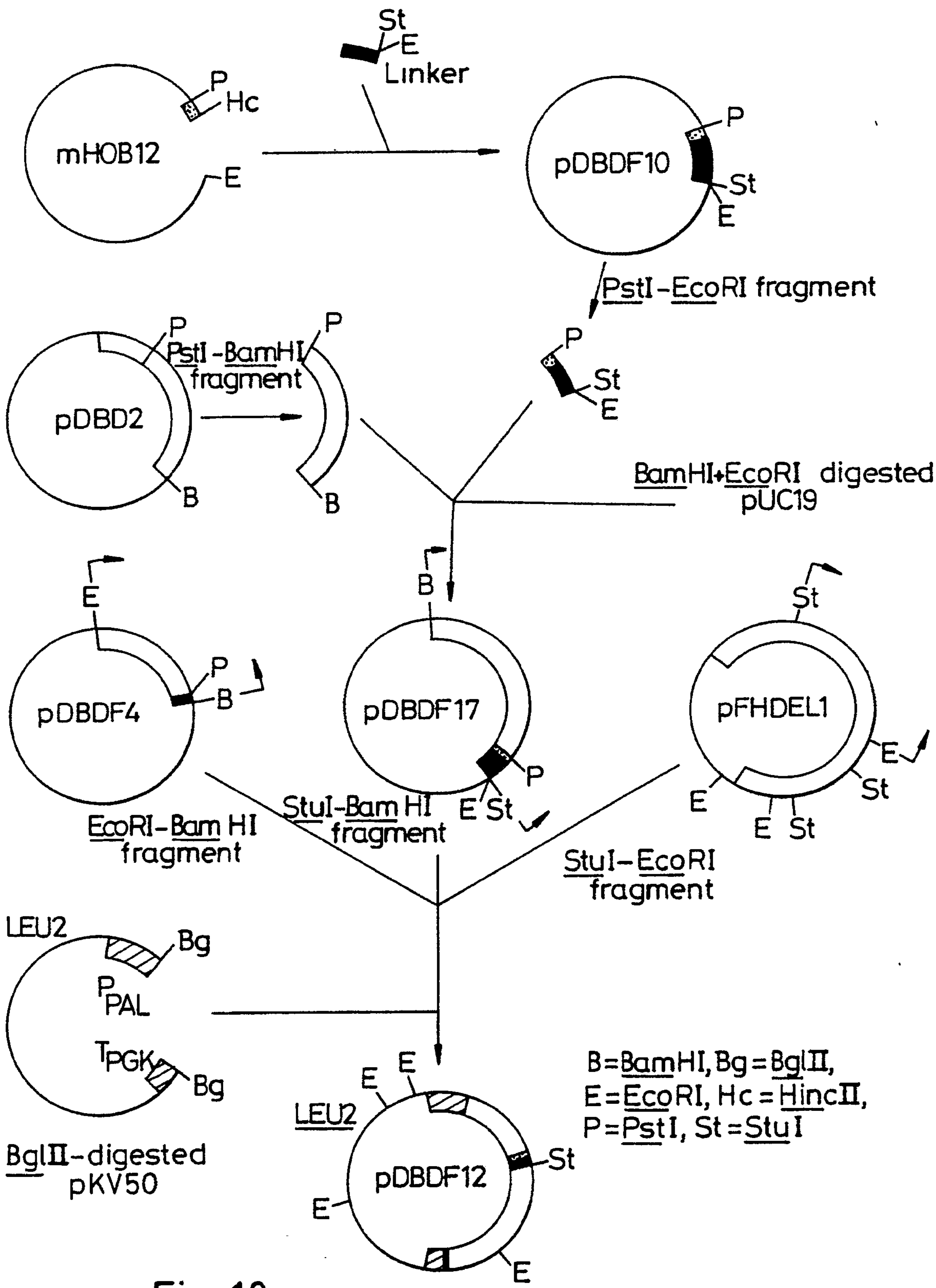
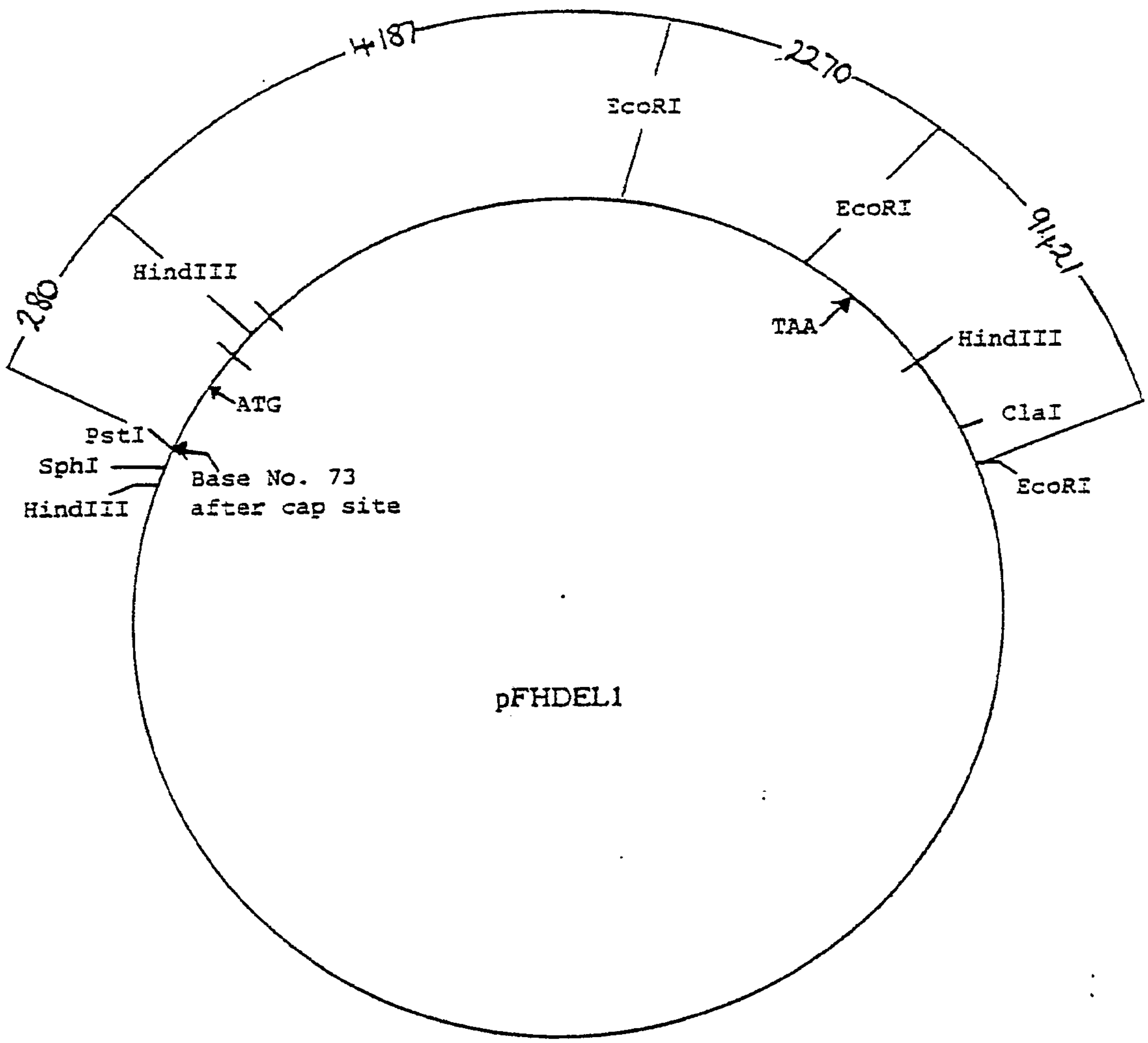


Fig. 10 Construction of pDBDF12

Figure 11

Name: pFHDEL1
Vector: pUC18 Amp^{fv} 2860bp
Insert: hFNcDNA ~ 7630bp



European Patent Office

EUROPEAN SEARCH REPORT

Application Number

EP 90 30 4575

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. Cl.5)
A	EP-A-0 308 381 (SKANDIGEN et al.)		C 12 N 15/62 C 07 K 13/00 C 12 P 21/02
T,D	EP-A-0 322 094 (DELTA BIOTECHNOLOGY LTD)		
			TECHNICAL FIELDS SEARCHED (Int. Cl.5)
			C 12 N C 12 P C 07 K

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
THE HAGUE	10-07-1990	VAN PUTTEN A.J.

CATEGORY OF CITED DOCUMENTS

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